



SEQUENCE LISTING

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YAN, TIE

<120> CHIMERIC GENE CONSTRUCTS FOR GENERATION OF FLUORESCENT
TRANSGENIC ORNAMENTAL FISH

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<140> 10/605,708
<141> 2003-10-21

<150> 09/913,898
<151> 2001-10-03

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<170> PatentIn Ver. 2.1

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Ser Val Thr Thr Val Ser Ser Lys Arg Tyr
490 495

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Gly Gly Tyr Gly Ser Gly Leu Gly Gly Leu Gly Gly Met Gly
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Phe Arg Cys Gly Leu Pro Ile Thr Ala Val Thr Val Asn Gln Asn Leu
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 Thr Ser Glu Lys Glu Gln Ile Lys Thr Phe Asn Asn Arg Phe Ala Phe
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 Gly Leu Gly Asn Glu Lys Met Lys Leu Glu Gly Glu Leu Lys Asn Met
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ttc aag ctg aac tac tca gtt gat gag gag tat cca gac ctt agc aag 160
Phe Lys Leu Asn Tyr Ser Val Asp Glu Glu Tyr Pro Asp Leu Ser Lys
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cac aac aac cac atg gcc aag gtg ctg act aag gaa atg tat ggc aag 208
His Asn Asn His Met Ala Lys Val Leu Thr Lys Glu Met Tyr Gly Lys
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ctt agg gac aag cag acc cca cct gga ttc act gtg gat gat gtc atc 256
Leu Arg Asp Lys Gln Thr Pro Pro Gly Phe Thr Val Asp Asp Val Ile
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cag act ggt gtt gac aat cca ggc cac ccc ttc atc atg acc gtc ggc 304
Gln Thr Gly Val Asp Asn Pro Gly His Pro Phe Ile Met Thr Val Gly
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Cys Val Ala Gly Asp Glu Ser Tyr Asp Val Phe Lys Asp Leu Phe
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cac aag acc gac ctc aac ttt gag aac ctg aag ggt ggt gat gac ctg 448
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Lys Gly Lys Tyr Tyr Pro Leu Lys Ser Met Thr Asp Asp Glu Gln Glu			
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Glu Met Glu Lys Lys Leu Gly Glu Gly Gln Ser Ile Asp Ser Met Ile
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cct gcc cag aag taa agcgggaggc cttccat ttccgt ctgtctgt 1271
Pro Ala Gln Lys
380

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Pro Gly Phe Thr Val Asp Asp Val Ile Gln Thr Gly Val Asp Asn Pro
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Gly His Pro Phe Ile Met Thr Val Gly Cys Val Ala Gly Asp Glu Glu
65 70 75 80
Ser Tyr Asp Val Phe Lys Asp Leu Phe Asp Pro Val Ile Ser Asp Arg
85 90 95
His Gly Gly Tyr Lys Ala Thr Asp Lys His Lys Thr Asp Leu Asn Phe
100 105 110
Glu Asn Leu Lys Gly Gly Asp Asp Leu Asp Pro Asn Tyr Phe Leu Ser
115 120 125
Ser Arg Val Arg Thr Gly Arg Ser Ile Lys Gly Tyr Pro Leu Pro Pro
130 135 140
His Asn Ser Arg Gly Glu Arg Arg Ala Val Glu Lys Leu Ser Val Glu
145 150 155 160
Ala Leu Ser Ser Leu Asp Gly Glu Phe Lys Gly Lys Tyr Tyr Pro Leu
165 170 175
Lys Ser Met Thr Asp Asp Glu Gln Glu Gln Leu Ile Ala Asp His Phe
180 185 190
Leu Phe Asp Lys Pro Val Ser Pro Leu Leu Ala Ala Gly Met Ala
195 200 205
Arg Asp Trp Pro Asp Ala Arg Gly Ile Trp His Asn Glu Asn Lys Ala
210 215 220
Phe Leu Val Trp Val Lys Gln Glu Asp His Leu Arg Val Ile Ser Met
225 230 235 240
Gln Lys Gly Gly Asn Met Lys Glu Val Phe Lys Arg Phe Cys Val Gly

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Leu Gln Arg Ile Glu Glu Ile Phe Lys Lys His Asn His Gly Phe Met		
260	265	270
Trp Asn Glu His Leu Gly Phe Val Leu Thr Cys Pro Ser Asn Leu Gly		
275	280	285
Thr Gly Leu Arg Gly Gly Val His Val Lys Leu Pro Lys Leu Ser Thr		
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His Ala Lys Phe Glu Glu Ile Leu Thr Arg Leu Arg Leu Gln Lys Arg		
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Gly Thr Gly Gly Val Asp Thr Ala Ser Val Gly Gly Val Phe Asp Ile		
325	330	335
Ser Asn Ala Asp Arg Ile Gly Ser Ser Glu Val Glu Gln Val Gln Cys		
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Ile Val Gly Ala Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg	
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Leu Ser Leu Arg Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met			
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Met Arg Lys Ala Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu			
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Arg Leu Leu Pro His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys			
80	85	90	
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Glu Asp Leu Thr Glu Val Arg Asp Leu Leu Ala Asn Lys Val Pro			
95	100	105	
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110	115	120	
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Ala Gln Asn Thr Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala			
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Leu Gly Ile Thr Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser			
145	150	155	
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Thr Leu Leu Asn Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr			
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225	230	235	
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Leu Ala Ser Ile Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu			
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Lys Ala Tyr Leu Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val			
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Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met Met Arg Lys Ala			
50 55 60			
Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu Arg Leu Leu Pro			
65 70 75 80			
His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys Glu Asp Leu Thr			
85 90 95			
Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro Ala Ala Ala Arg			
100 105 110			
Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro Ala Gln Asn Thr			
115 120 125			
Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala Leu Gly Ile Thr			
130 135 140			
Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser Asp Val Gln Leu			
145 150 155 160			
Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala Thr Leu Leu Asn			
165 170 175			
Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr Gly Leu Ile Ile			
180 185 190			
Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro Glu Val Leu Asp			
195 200 205			
Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys Gly Val Arg Asn			
210 215 220			
Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr Leu Ala Ser Ile			
225 230 235 240			
Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu Ala Val Thr Val			
245 250 255			
Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val Lys Ala Tyr Leu			

260	265	270
Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val Ala Ala Ala Thr		
275	280	285
Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu Ala Pro Lys Glu		
290	295	300
Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly Leu Phe Asp		
305	310	315

<210> 7
<211> 2241
<212> DNA
<213> Danio rerio

<220>
<221> TATA signal
<222> (2103) .. (2108)

<220>
<221> primer bind
<222> (2221)_.(2241)
<223> CK2

<220>
<221> misc feature
<222> (2142) .. (2235)
<223> Identical to the 5' CK cDNA

<400> 7
ccttcccttc tactttgac gtcctttaa gattactcat ctcaaacacc catacaaagg 60
tcacacctgg tttatactat gatagttgtc cagtgcgtgc tgtgacaccc aactgctgcc 120
aattgtctga ctatcgagg tgcgtatgcg tatagttac agtttagacca aagtgtgctg 180
gtgtgtgaag taacaaatga caaatactca aattgttaatt tactaagttag tttaaaaatg 240
tagtgcagtgtt ttggacttt tatttcactt ttattcttgt ctatgtggat tagacaaatc 300
acatagaagg taaatcacat cataatgaac agcaaactgt ttgcgcgat taaaagaaga 360
agactgctta gatgcgtgtc actgtatgaga aaataacttt aaacgcacac aagacggcac 420
gtaccccaac gcagtgggaa cggtgcattt gaactcaacg tcaggtcgat gtcaatgttc 480
ctaattgtatgt tacagcttgc tggttatgcgg ggattatggat tgccataacct gatgaaataaa 540
ggttcgacat tggattttgg tcgccttcca cctatgacat cggttattggat cgtaaaaata 600
aatttaggtc accacaacccat atatttaacc tgctggcaa taactaaatg cactacagaa 660
taaatgcacat agctttcac agcataatac aaaagctact ttctactcat actttgagta 720
acatttttag gcatgtatttgc atattttcac cagccctccc catacataat cgatgttta 780
acatttagctt tgtagccgc tagcattact gagcttgatc atgaaaggcag atttgagact 840
gatgattgcc gtaccatgtat ctcacacccat gacgattgcg taatgtctatt aaatgcccatt 900
atttcgtgtt gacttgcacg agaaatgaga tggaaacatt tatcagtggat cattaaatac 960
tatttttgtt ttagcttgc tgcatgtttt aactattgtat attaagttagt ttttctcaga 1020
tgacttttgc ctttcccttg agtacatttt ctttccttca acctgcgttc actactttat 1080
agtccctgtga ttccctgttcca atcaaattgc taccttaaga catggccat ttataattgc 1140
tgtcaaaaat atttacacgc attaacccatg agatgtatggat tggttactgt atgatgaccg 1200
aagacgtcaa catggcgat ggttgcgtt tggttagaaaa tgaaaatttag gttgacgtca 1260
aacatccaaat ctaaaatcat atatcaatgtt atgttacccat tatgacgtct atcagacgtt 1320
tgtcattatt tgacgttgg ttaagatgtt acacaaccta aatccaccaa atattaactt 1380
acaatatccat tagatgtgg ctagacttttgc taatattaac atctttagat gttgtgtgcc 1440
tggtagtgc acacacatgtt aaattacatgt tcactactta ctactcttgc gtactttaa 1500
atatttacaaat ctgataactt tactcgact tatgattttt cagtagtgc tccactactg 1560
cacatatggat gtagtttgc ggcataatct gtgcagaattt gttgtgtgc acattttcca 1620
atatcaatac agaaggaaac tggtagtgc gttcccttgc aatctcaac aatgcacgtt 1680

ttcagctcag gggaaaaat gccctgccag atccaaacgg ctggcaaaag tgaatggaaa 1740
aaagccttc attaatgtga aagttgctgc gcgc(ccc)acc cagataaaaaa gagcagagg 1800
taacatgctc tctacggctg tccagccaac caga(tact)ga ggcagaaaaca cacc(cgt)gg 1860
cagatggtga gagtacact gtctttcca gagtttctac tggaatgcct gtcctcaagt 1920
ctcaaggcctc tccttgcatt ctctcattcc acctggggca aagccccagg ctgggtgtga 1980
caacatttat cttaccactt tctctctgta cctgtcta(ac aggttagggtg tgtgtgagag 2040
tgcgtatgtg tgcaagtgcg tgtgtgtgt agagcagtca gctccaccct ctcaagagt 2100
tgtataaaaat tggtcagcca gctgctgaga gacacgcaga gggactttga ctctcctttg 2160
tgagcaacct cctccactca ctccctctc agagagcact ctcgtacctc cttctcagca 2220
actcaaagac acaggatccg g 2241

```
<210> 8  
<211> 1456  
<212> DNA  
<213> Danio rerio
```

<220>
<221> TATA signal
<222> (1389)..(1394)

<220>
<221> primer bind
<222> (1433)_.(1456)
<223> MCK2

```
<220>
<221> misc feature
<222> (1428)..(1453)
<223> Identical to the 5' MCK cDNA
```

<400> 8
gaattgcaaa gtcagagtaa taaaatgaaa ccaaaaaaca tttttaaata tacttgtctc 60
tgtggcttaa tctggctga tgtgtgtgtg tgtgtgtgt tacttgacag ctgctagtga 120
gcatgtgcac catgacaggc ctgttattca cacttgggtgc catgtggag actgttcggc 180
cagctatagt tttttccaca gagtcctggg tcacctaatt tcacaaggaa gaaacatgtt 240
acatgttaaa atgtgacatt caaattgttag tgccattactt aacgaaacgc attacacaag 300
ttacagctta aaagattgct agacagaaaa accagggagg ggtttccca taatatccag 360
tgagactcta ggagcgggaa cactaacagg cctccctgag tgagaacatt gcatgtgcgc 420
gtgacagaaa accagagatg gaaatacctt ctttgaatt gcataattgc taaaagaag 480
acacaacagg gatagttcac ccaaaaaaca gaccattctt ttttctgtt gaacaaaaat 540
taagatattt tgaagaatgc ttaccgaata acttccatata ttggaaacta attacagtga 600
aagtcaatgg gtcttccagc atttttcaa tataccttac tttgagttca aaagaaaaac 660
acatctaaa taggttttag gttgaataaa cattttcat tttggggtagt actatcccta 720
attatttgac acttaagatt tatagtaaat cattttatacg actttctccc cttattaaac 780
atggttgaat ttatcttcat gttttagtgc ggggtgtgct tttttgaaaa gatttccctg 840
tcaaatgttt ttgtgtatgg ttggcgcaca atagactgaa ctggccatc acacagactt 900
tcataacaac tccagtttat gcccttcac cctcagtgtat taaaatatggc gtctgacatg 960
agcagattaa acacgacact gcaacaactt tacctgtaaa aatacaaatt gagttgcac 1020
ccagaatcat gtggtaacg aagcctacca agagattttt gaaagccatc ggcctgacac 1080
gcbcacttct gatatctgtg gtatgtttgg caaaagtgc gtcagccctt ttagcatgg 1140
cagatccccc acatccccatc accccctcctt caacctattc cctcctggaa agctatgtat 1200
ggggcgggaa gtgtaaatgg atatggaaag gaaggggggc accacccaca gctgccacct 1260
catctaggat gcctggggcc taaattgaag cctttcttac actaaacagg gcataagaga 1320
ccagcgccag ccaatcataa ttcaagtggc tctaaaatgg gccagccaat ggctgcaggg 1380
gctagaggtt tatatatcca aatcaaactc ttcttgctt ggtgaccctt atttcggctt 1440
ggtaacagg atccgg 1456

<210> 9
<211> 2205
<212> DNA
<213> Danio rerio

<220>
<221> primer bind
<222> (2179)..(2205)
<223> ARP2

<220>
<221> misc_feature
<222> (2153)..(2199)
<223> Identical to the 5' ARP cDNA

<220>
<221> intron
<222> (792)..(2152)

<220>
<221> misc_feature
<222> (775)..(791)
<223> Identical to the 5' ARP cDNA

<400> 9
atctgtatta agaaacactt aaaatatata tgcgttacga attaaaaaca aaacacgatc 60
atttaattt gtgttgtata attttacatt ttgttaagtat tattttata aaaaatata 120
agaaataata caaatttggt tacagtattc ttagttattg caataaacga attttatata 180
gaaagagaaaa gagtttatt ataagatgtt caatttaaaa aatggcagaa aatagaaaaaa 240
tgattgtcaa gatgataaaa gtcagtttag acaaaaaaaaat aagatgaaaa acatcaaaaat 300
agataataaaa gtgactttt tgggcggacc aaattccct attaatggtc aattcattaa 360
aatacattca ttaaaataaa ggtattgcga tgaattttaga tgcacagtgta ttttggttct 420
gtgcagattt ttggctgtt ttagaaggga tacatctgcg gccgaaagg aacgggaact 480
atttacattc tttgcttatta aattatccat tattttgtatt ttattacccc aaccgtaaac 540
tcaaccctca cagtaatgtt aaaaatattt ttattttt atagcgtaac agaatgatgc 600
tatattgacc gcagctgtat cctttctaag tgcgactgtt caaatacgca ctgaccgtga 660
cagacacgtg cattgaccaa tcagcgcaca gatacgcatt ttccgcgcga ttctgattgg 720
atgatcgact gatactaata ttgtgccgt tcctttcgcg gccttttct ttcacgcgtc 780
cctaccgtga ggttaaggctg acgcccgtct tggcgggtt tcttaaaatg tgttaataaa 840
taacatcata agaggtcact agaaggcttca cgtgttttta atatcagcgg cggttattat 900
tatgcgttta aagcttgtt aatgattttt acagtaaaaag ttagcactag cctgttagca 960
caggcctcgt gcgcattgtt tgacgcgacg tttaatagc atcttattt atttgtatga 1020
tccgattctg atattaatca tattttatgcg taaaatgtgt gatgggtctg ctatggaca 1080
ttacatgcta gtacttgtc tagtcggcgt atccacattt agatgttgcg ctatttgcctt 1140
tttaaaacc agttactctc attttatgtt aatattcttta agccactaag ttaaaatttt 1200
tcaatcacat ataattgtgt ttatgtttt tttgagtcat cataccaggt aatagtttta 1260
tttatattat tatgtacaat ttggcataaa ctgccttcgg ttttggattga catctacttt 1320
gtaaaggtaa tcttaaaagggtt gtaaaggctc accaaaaaga caattcaccg tcaagtgttt 1380
tcaaataatctt tgagttctt aatgaacatg gtatgtttt gagaacttgc gaaaccaact 1440
accataatac aaatacagga aaaaataact atagaagtgc atggttacag gtttctgca 1500
ttcaaaaatctt acacacaagt gtttaatggg aggaactcaa gtgatttggaa aagtttaagg 1560
tgctataatc agtttcatt tgggtgagct gtctctaaac atttgatttta gacacccctc 1620
gcagtggtca ccaagctgtt tcctgaaggcc gcaatgttcc acagattttt gctccaaccc 1680
taattaaaca cacctgaaca agctaataa ggtcttacta ggtatgtttt gaaatccatcc 1740
gcaggtgtgt tggatgttcaaga tagagctaa ccctgcaggcc acaatggccc aacaggattt 1800
gtgaccccttgc cctcaagcca tcacaaatgc attatgttta taagaaatgtt gcaggttcag 1860

ttatggacag gctgttcag tgcttgcac tcgcccac tgcacaaatg aacatgattc 1920
cttctatccc tgtctgtctg catctcatga cttgcaggga cgctggctc agacacgtt 1980
atagcagtaa atcaaataca atagtgcctt gattatctt aaatatttga aagcttataa 2040
taggcaacca aattacctgg aaacagttt caaacagtaa ttcatatctt gtcatttaat 2100
aagatgcaca caaggcaggta gtaaaagtt tgcttgtt tgtaatccctc agatttaca 2160
accttgcctt taaaccggct gttcacccat ctttggagg gatcc 2205

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cytokeratin - gene specific primer

<400> 10
cgctggagta agagatagac ctgg 24

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cytokeratin gene specific primer

<220>
<221> misc feature
<222> (1)..(6)
<223> Introduced for restriction site

<220>
<221> misc feature
<222> (3)..(8)
<223> BamHI site

<400> 11
ccggatcctg tgtcttgag ttgctg 26

<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Muscle creatine kinase gene specific primer

<220>
<221> misc feature
<222> (3)..(8)
<223> BamHI site

<400> 12

ccggatcctt gggatcagat cctg

24

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Muscle creatine kinase gene specific primer

<220>
<221> misc feature
<222> (1)..(3)
<223> Introduced for restriction site

<220>
<221> misc feature
<222> (3)..(B)
<223> BamHI site

<400> 13
ccggatcctg ttcaccaagg cgaa

24

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Acidic ribosomal protein PO gene specific primer

<400> 14
tagttggact tccacgtgcc ctgtc

25

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Acidic ribosomal protein PO gene specific primer

<220>
<221> misc feature
<222> (1)..(7)
<223> Introduced for restriction site

<220>
<221> misc feature
<222> (1)..(6)
<223> BamHI site

<400> 15
ggatcccttc caaggatcg tgaaca 26

<210> 16
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide for linker used in linker-mediated PCR

<400> 16
gtcatcttt acaagcttagc gctgaacaat gctgtggaca agcttgaatt c 51

<210> 17
<211> 10
<212> DNA
<213> Artificial Sequence

<223> Description of Artificial Sequence:
Oligonucleotide for linker used in linker-mediated PCR

<220>
<221> misc_feature
<222> (10)..(10)
<223> n is a dideoxycytidine

<400> 17
gaattcaagn 10

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
linker specific primer

<400> 18
gtcatcttt acaagcttagc g 21

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
linker specific primer

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<400> 19
tcctgaacaa tgctgtggac                                20

<210> 20
<211> 1392
<212> DNA
<213> Danio rerio

<220>
<221> CDS
<222> (42)..(551)

<220>
<221> primer bind
<222> (6)..(28)
<223> M2

<220>
<221> primer bind
<222> (23)..(45)
<223> M1

<220>
<221> polyA signal
<222> (797)..(802)

<220>
<221> polyA_signal <222> (1351)..(1357)

<400> 20
ctttcttga tcttcttaga cttcacat accgtctcga c atg gca ccc aag aag 56
                                         Met Ala Pro Lys Lys
                                         1                      5

gcc aag agg agg gca gca gga gga gag ggt tcc tcc aac gtc ttc tcc      104
Ala Lys Arg Arg Ala Ala Gly Gly Glu Ser Ser Asn Val Phe Ser
                                         10                  15                  20

atg ttt gag cag agc cag att cag gag tac aaa gag gct ttc aca atc      152
Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys Glu Ala Phe Thr Ile
                                         25                  30                  35

att gac cag aac aga gac ggt atc atc agc aaa gac gac ctt agg gac      200
Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys Asp Asp Leu Arg Asp
                                         40                  45                  50

gtg ttg gcc tca atg ggc cag ctg aat gtg aag aat gag gag ctg gag      248
Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys Asn Glu Glu Leu Glu
                                         55                  60                  65

gcc atg atc aag gaa gcc agc ggc cca atc aac ttc acc gtt ttc ctc      296
Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn Phe Thr Val Phe Leu
                                         70                  75                  80                  85

acc atg ttc gga gag aag ttg aag ggt gct gac ccc gaa gac gtc atc      344
Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp Pro Glu Asp Val Ile

```

90	95	100	
gtg tct gcc ttc aag gtg ctg gac cct gag ggc act gga tcc atc aag			392
Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly Thr Gly Ser Ile Lys			
105	110	115	
aag gaa ttc ctt gag gag ctt ttg acc act cag tgc gac agg ttc acc			440
Lys Glu Phe Leu Glu Leu Leu Thr Thr Gln Cys Asp Arg Phe Thr			
120	125	130	
gca gag gag atg aag aat ctg tgg gcc gcc ttc ccc cca gat gtg gct			488
Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe Pro Pro Asp Val Ala			
135	140	145	
ggc aat gtt gac tac aag aac atc tgc tac gtc atc aca cac gga gag			536
Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val Ile Thr His Gly Glu			
150	155	160	165
gag aag gag gag taa acaacttgg aatagaggaa acgaagagaa gaacatgcat			591
Glu Lys Glu Glu			
170			
cctcacagct taatctccag tctgttgtct ggcccttctct aactttgtt tttccttcct			651
ccctttcttg ctttctacca tcgttgttac tccaagcact tacactctcc atcttaccaa			711
agacttgtct cgctgggact gaattgggag ggtggagagg aacacgacca cagtgtctgt			771
cgagtgggga catgggattt tttcaataa aatgaacatc atttctgtat ctctcacatt			831
ctctctttct ctctgtttct cactcattac ccacaacccc tctctttcat ttcagtcaag			891
cttgcatgta agtcgctgct tcttctgctg cagtcttagg agttgaaacg aaggcatcta			951
tagtttgggg ctgaaaacatc tctctagatc aatgtggaag agtgctact ctgagggggaa			1011
aagaagcacg atggagtgtat ctcactctat aatagaggaa ccagtcatca ttctcatttc			1071
ctcctctggt ggttactaa aaagagaaag agaaaatgag ggttttgtgc tgagtgagtt			1131
tagcctccta aaagcgatgc cgagctcatc acagagggag tgagagggac agaccatcct			1191
aggaagagag gagagcaggg actgaaagaa aacataacct cttcactccc cctctccct			1251
cctcttctct atttctctgt ccatctttc tttttcttt tttcttttt gctttctgca			1311
tctgggcctg ctttgctctg ccaaaccctct cctgttaacca ataaaaagac acaaactgtg			1371
aaaaaaaaaa aaaaaaaaaa a			1392

<210> 21
 <211> 169
 <212> PRT
 <213> Danio rerio

<400> 21
Met Ala Pro Lys Lys Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser
1 5 10 15
Ser Asn Val Phe Ser Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys
20 25 30
Glu Ala Phe Thr Ile Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys
35 40 45
Asp Asp Leu Arg Asp Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys
50 55 60
Asn Glu Glu Leu Glu Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn
65 70 75 80
Phe Thr Val Phe Leu Thr Met Phe Gly Glu Leu Lys Gly Ala Asp
85 90 95
Pro Glu Asp Val Ile Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly
100 105 110
Thr Gly Ser Ile Lys Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln
115 120 125
Cys Asp Arg Phe Thr Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe
130 135 140
Pro Pro Asp Val Ala Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val
145 150 155 160
Ile Thr His Gly Glu Glu Lys Glu Glu
165

<210> 22
<211> 2054
<212> DNA
<213> Danio rerio

<220>
<221> TATA signal
<222> (1983)..(1989)

<220>
<221> enhancer
<222> (142)..(148)
<223> E-box, canntg

<220>
<221> enhancer
<222> (452)..(457)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1095)..(1100)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1278)..(1283)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1362)..(1367)

<223> E-box, canntg

<220>
<221> enhancer
<222> (1385)..(1390)
<223> E-box, canntg

<220>
<221> enhancer
<222> (523)..(532)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (606)..(615)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (697)..(706)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (1490)..(1499)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (1640)..(1649)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (1956)..(1965)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<223> Transcription start site at residue 2012

<220>
<221> primer bind
<222> (2032)..(2054)
<223> M2

<220>
<221> misc difference
<222> (2027)..(2054)
<223> Identical to the 5' MLC2f cDNA

<400> 22
tgcattgcctg gcaggtccac tcttagaggac tactagtcat atgcgattct gaacaatgct 60
ggaatgagcc accaactcat ccagtgtatt accctacact gggaaacacc caaatctgtc 120
tggttatattt gtgcataatac attagattag aagctgtcac tgcgggtgta ccttttcaaa 180
ttgatacctc aaaagtatat attagtcct tttaggtact aatataacc cttgaggttt 240
tcatttggaa aggtaccacc ccagtgcac ag aatctggag cttatccaac aaaataactt 300
tatttatatac ttattgaaaa atattaaata agcaaaaacaa tggaaaaaaa tttagttcaaa 360

atttagctt atttaaattg ttttatctt aatatagctg ttaataaaat ctgtttgtt 420
actgagagat ggagaaaaat attcatttc ctgttaattat ctgttttct aggtactgta 480
caagcaggag caaaaacaagc cgacagactc gggaatgcac aacaaactca agggggcaa 540
gagagcaagg agcgctcaag attgttagc ctgcctccc aaaaaaaaaac tgtcttaagc 600
caaccactca gaggcgtga gtgtgctgac cgtgctgac cacagggcag cttccacaa 660
gtgagggtcat aggtcgatcg gcagagagag atggcatgg ccatgtggac ggggtgtgg 720
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